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# OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 2.37576 Seconds

(without alignments)  
977.656 Million cell updates/sec

Title: US-09-988-971-2\_COPY\_35\_90

Perfect score: 288

Sequence: 1 ATATVALGSPAGGPAELSLR.....VLSEVSGREVNIPSHVAKV 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	35.1	511	1 LYN_MOUSE	P25911 mus musculus
2	101	35.1	511	1 LYN_RAT	Q07014 ratius norv
3	100	34.7	504	1 BLK_HUMAN	P51451 homo sapien
4	97	33.7	498	1 BLK_MOUSE	P16277 mus musculus
5	95	33.0	511	1 LYN_HUMAN	P07948 homo sapien
6	92.5	32.1	531	1 SRC2_XENLA	P13116 xenopus lae
7	90.5	31.4	509	1 STK_HYDAT	P17713 hydra atten
8	90	31.2	503	1 HCK_RAT	P50545 ratius norv
9	90	31.2	504	1 HCK_MACFA	Q95m30 mus musculus
10	90	31.2	526	1 HCK_HUMAN	P08631 homo sapien
11	89.5	31.1	531	1 SRC1_XENLA	P13115 xenopus lae
12	89.5	31.1	2415	1 SPCX_DROME	P13395 drosophila
13	89	30.9	507	1 LCK_CHICK	P42683 gallus gall
14	88	30.6	508	1 LCK_HUMAN	P06239 homo sapien
15	88	30.6	508	1 LCK_MOUSE	P06240 mus musculus
16	88	30.6	524	1 HCK_MOUSE	P08103 mus musculus
17	87.5	30.4	526	1 SRC_AVISR	P00525 avian sarco
18	87.5	30.4	526	1 SRC_RSVH1	P25020 rous sarcom
19	87.5	30.4	526	1 SRC_RSVH1	P25020 rous sarcom
20	87.5	30.4	532	1 SRC_CHICK	P00526 rous sarcom
21	87.5	30.4	532	1 SRC_AVIST	P00523 gallus gall
22	87.5	30.4	568	1 SRC_AVISS	P14085 avian sarco
23	87.5	30.4	587	1 SRC_AVIS2	P14084 avian sarco
24	86.5	30.0	537	1 YES_XENLA	P15054 avian sarco
25	86.5	29.7	535	1 SRC_HUMAN	P10936 xenopus lae
26	85.5	29.7	535	1 SRC_HUMAN	P10931 homo sapien
27	85.5	29.7	536	1 FYN_XIPHE	Q9w496 ratius norv
28	85.5	29.7	1113	1 MTSB_IDCD1	P27446 xiphophorus
29	84.5	29.3	543	1 YES_HUMAN	P34109 dicyostell
30	83.5	29.0	533	1 FYN_MOUSE	P07947 homo sapien
31	83.5	29.0	536	1 FYN_HUMAN	P33688 mus musculus
32	83	28.8	528	1 SEM5_CAEBL	P06241 homo sapien
33	82.5	28.6	382	1 YH6_YEAST	P23355 caenorhabd

34	82.5	28.6	536	1 FYN_XENLA	P13406 xenopus lae
35	82.5	28.6	539	1 YES_CANFA	Q28923 canis fam1
36	82.5	28.6	540	1 SRC_MOUSE	P05460 mus musculus
37	82.5	28.6	541	1 YES_CHICK	P09324 gallus gall
38	82.5	28.6	2418	1 SPCX_HUMAN	P02549 homo sapien
39	81.5	28.3	373	1 YFJ4_YEAST	P43603 saccharomyc
40	81.5	28.3	526	1 SRC_RSVH1	P00524 rous sarcom
41	81.5	28.3	535	1 YRK_CHICK	Q02927 gallus gall
42	80.5	28.0	528	1 YES_AVISR	P00527 avian sarco
43	80.5	28.0	541	1 YES_MOUSE	Q04736 mus musculus
44	80.5	28.0	2472	1 SPCN_HUMAN	Q13813 homo sapien
45	80.5	28.0	2472	1 SPCN_RAT	P16086 ratius norv

## ALIGNMENTS

RESULT 1  
LYN\_MOUSE STANDARD; PRT, 511 AA.  
AC P25911; Q62127;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).  
GN LYN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP MEDLINE=91260688; PubMed=1710766;  
RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,  
RA Lock P., Dunn A.R.;  
RT "Alternatively spliced murine lyn mRNAs encode distinct proteins.";  
RL Mol. Cell. Biol. 11:3399-3406(1991).  
RN [2]  
RP MEDLINE=91203857; PubMed=2017160;  
RA Yi T., Bolen J.B., The J.N.;  
RT "Hematopoietic cells express two forms of lyn kinase differing by 21  
RT amino acids in the amino terminus.";  
RL Mol. Cell. Biol. 11:2391-2398(1991).  
RN [3]  
RP MEDLINE=90152381; PubMed=2482828;  
RA Milke A.F., Kurban R.R., Hovens C.M., Ralph S.J.;  
RT "The application of the polymerase chain reaction to cloning members  
RT of the protein tyrosine kinase family.";  
RL Gene 85:67-74(1989).  
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -I- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND  
CC MYELOID CELLS.  
CC -I- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
CC SUBFAMILY.  
CC -I- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
CC EMBL: M64608; AAA9470.1; -  
CC EMBL: M57696; AAA9471.1; -  
CC EMBL: M57697; AAA9472.1; -  
DR EMBL; M57697; AAA9472.1; -

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DR EMBL, M33426; AAA40017.1; -.
DR PIR, A39719; A39719.
DR HSSP, P08631; 1AD5.
DR MGD; MG1:96892; LYN.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR01452; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR PROTO-ONCOGENE; Tyrosine-protein kinase; Phosphorylation;
KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
KW Palmitate; Lipoprotein; Alternative splicing.
FT INIT MET 0
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT DOMAIN 2 2 PALMITATE (BY SIMILARITY).
FT DOMAIN 62 122 SH3.
FT DOMAIN 128 225 SH2.
FT DOMAIN 246 500 PROTEIN KINASE.
FT NP_BIND 252 260 ATP (BY SIMILARITY).
FT BINDING 274 274 ATP (BY SIMILARITY).
FT ACT_SITE 366 366 BY SIMILARITY.
FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARSPIC 507 507 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 24 44 MISSING (IN ISOFORM LYN B).
FT CONFLICT 76 76 I -> F (IN REF. 2).
FT CONFLICT 160 160 P -> L (IN REF. 2).
FT CONFLICT 278 278 F -> L (IN REF. 2).
FT CONFLICT 390 390 V -> I (IN REF. 2).
FT CONFLICT 414 414 I -> F (IN REF. 3).
FT CONFLICT 424 424 D -> N (IN REF. 1).
FT CONFLICT 431 431 L -> P (IN REF. 3).
SQ SEQUENCE 511 AA; 58681 MW; 3935221CC9C50F0 CRC64;

Query Match 35.1%; Score 101; DB 1; Length 511;
Best Local Similarity 43.4%; Pred. No. 0.00049;
Matches 23; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Cy 4 VALGFPAGPAELSLRLGPLTIVSEDDMTLSEVSGREYNIPSVHAKV 56
Db 68 VALPYDGIHPDDLSFKKGGKMKVLEHGEHWKAKSLSSKREGFIPSNVAKV 120

RESULT 2
LYN_RAT STANDARD; PRT; 511 AA.
AC 007014; O63320;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
GN LYN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Minoguchi K., Nishikata H., Siraganian R.P.;

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RT "Bacterially expressed rat p56lyn binds several proteins in rat
RT basophilic leukemia cells including pp72, a tyrosine phosphorylated
RT protein prominent in activated cells.";
RL J. Immunol. 150:222-222(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94171041; PubMed=8125304;
RA Rider L.G., Raden N., Miller L., Telsma C.;
RT "The cDNA encoding two forms of the LYN protein tyrosine kinase are
RT expressed in rat mast cells and human myeloid cells.";
RL Gene 138:219-222(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442484; PubMed=9295361;
RA Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
RT "The unique domain as the site on LYN kinase for its constitutive
RT association with the high affinity receptor for IgE.";
RL J. Biol. Chem. 272:24072-24080(1997).
CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1 TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
CC MYELOID CELLS.
CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC -1 SUBFAMILY.
CC -1 SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, L14951; AAA41549.1; -.
DR EMBL, L14782; AAA20944.1; -.
DR EMBL, L14823; AAA20945.1; -.
DR EMBL, AF000300; AAB71344.1; -.
DR EMBL, AF000301; AAB71345.1; -.
DR EMBL, AF000302; AAB71346.1; -.
DR HSSP, P08631; 1AD5.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; Tyr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW PROTO-ONCOGENE; Tyrosine-protein kinase; Phosphorylation;
KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
KW Palmitate; Lipoprotein; Alternative splicing.
FT INIT MET 0
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT LIPID 2 2 PALMITATE (BY SIMILARITY).
FT DOMAIN 62 122 SH3.
FT DOMAIN 128 225 SH2.
FT DOMAIN 246 500 PROTEIN KINASE.

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FT NP BIND 252 260 ATP (BY SIMILARITY).  
 FT BINDING 274 274 ATP (BY SIMILARITY).  
 FT ACT\_SITE 366 366 BY SIMILARITY.  
 FT MOD\_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).  
 FT VARSPLIC 24 44 MISSING (IN ISOFORM LYN B).  
 FT CONFLICT 230 230 P -> L (IN REF. 2).  
 FT CONFLICT 307 307 V -> A (IN REF. 2).  
 FT CONFLICT 418 418 C -> Y (IN REF. 2).  
 SQ SEQUENCE 511 AA, 58529 MW, 242255229CD43ED CRC64;

Query Match 35.1%; Score 101; DB 1; Length 511;  
 Best Local Similarity 43.4%; Pred. No. 0.00049;  
 Matches 23; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 4 VALGSPAGPAEILRLRGLTIVSEDDGMWTVLSVSGRENNPSVYAKV 56  
 DB 68 VALPYDGHDDLSFKGKGMKVLEHSGEMWAKSLSSKKEGIFPSYVAKV 120

RESULT 3  
 ID BLK\_HUMAN STANDARD; PRT; 504 AA.  
 AC P51451; O16291;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-BLK).  
 GN BLK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95123078; PubMed=7822795;  
 RA Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.;  
 RT "Molecular cloning, characterization, and chromosomal localization of  
 a human lymphoid tyrosine kinase related to murine Blk.";  
 RL J. Immunol. 154:1265-1272(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95148218; PubMed=7845672;  
 RA Diebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,  
 RA Niederhuber J.E.;  
 RT "Molecular cloning and chromosomal localization of the human homologue  
 of a B-lymphocyte specific protein tyrosine kinase (blk).";  
 RL Oncogene 10:477-486(1995).  
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT  
 IS RESTRICTED TO B LYMPHOID CELLS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; Z33998; CAA83965.1; -;  
 DR EMBL; S76617; AAB33265.1; -;  
 DR HSSP; P16277; BLK.  
 DR Genew; HGNC:1057; BLK.  
 DR MIM; 191305; -;  
 DR InterPro; IPR000719; Euk\_Pkinase.  
 DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_Pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrcK; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE\_TYR\_FALSE\_NEG.  
 DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;  
 KW Myristate; SH2 domain; SH3 domain.  
 FT INIT MET 0  
 FT LIPID 1 1  
 FT DOMAIN 57 117  
 FT DOMAIN 123 219  
 FT DOMAIN 240 493  
 FT NP\_BIND 246 254  
 FT BINDING 268 268  
 FT ACT\_SITE 359 359  
 FT MOD\_RES 388 388  
 FT CONFLICT 286 286  
 FT CONFLICT 406 406  
 SQ SEQUENCE 504 AA; 57607 MW; BD1DF50ECTJ370C8 CRC64;

Query Match 34.7%; Score 100; DB 1; Length 504;  
 Best Local Similarity 41.5%; Pred. No. 0.00062;  
 Matches 22; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 4 VALGSPAGPAEILRLRGLTIVSEDDGMWTVLSVSGRENNPSVYAKV 56  
 DB 63 VALDYTNANDRDLOMLKGEKVLKGTGDMWLARSLVTRGSGVPSNFVAKV 115

RESULT 4  
 ID BLK\_MOUSE STANDARD; PRT; 498 AA.  
 AC P16277;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-BLK).  
 GN BLK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISUS-B-cell;  
 RC MEDLINE=90117147; PubMed=2404338;  
 RA Dymecki S.M., Niederhuber J.E., Desiderio S.V.;  
 RT "Specific expression of a tyrosine kinase gene, blk, in B lymphoid  
 cells.";  
 RL Science 247:332-336(1990).  
 RN [2]  
 RP STRUCTURE BY NMR OF SH2 DOMAIN.  
 RA MEDLINE=96224819; PubMed=8639560;  
 RA Metzler W.J., Letting B., Pryor K., Mueller L., Farmer B.T. II;  
 RT "The three-dimensional solution structure of the SH2 domain from  
 p55blk kinase.";  
 RL Biochemistry 35:6201-6211(1996).  
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT

CC IS RESTRICTED TO B LYMPHOID CELLS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC  
 CC EMBL; M30903; AAA40453.1; -  
 CC PIR; A40092; A40092.  
 CC PDB; 1BLJ; 12-MAR-97.  
 CC PDB; 1BLK; 12-MAR-97.  
 CC MGI; MGI:88169; BIK.  
 CC InterPro; IPR000719; Euk\_pkinase.  
 CC InterPro; IPR000980; SH2.  
 CC InterPro; IPR01452; SH3.  
 CC InterPro; IPR01245; Tyr\_pkinase.  
 CC Pfam; PF00017; SH2; 1.  
 CC Pfam; PF00018; SH3; 1.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00401; SH2DOMAIN.  
 CC PRINTS; PR00452; SH3DOMAIN.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Euk\_pkinase; 1.  
 CC ProDom; PD000066; SH3; 1.  
 CC ProDom; PD000093; SH2; 1.  
 CC SMART; SMO0252; SH2; 1.  
 CC SMART; SMO0326; SH3; 1.  
 CC SMART; SMO0219; TYRC; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00109; PROTEIN\_KINASE\_TYR; FALSE\_NEG.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE; PS50001; SH2; 1.  
 CC PROSITE; PS50002; SH3; 1.  
 CC Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;  
 CC Myristate; SH2 domain; SH3 domain; 3D-structure.  
 CC MYRISTATE (BY SIMILARITY).  
 CC LIPID 1 111 SH3.  
 CC DOMAIN 51 111 SH3.  
 CC DOMAIN 117 213 SH2.  
 CC DOMAIN 234 487 PROTEIN KINASE.  
 CC NP\_BIND 240 248 ATP (BY SIMILARITY).  
 CC BINDING 262 262 ATP (BY SIMILARITY).  
 CC ACT\_SITE 353 353 BY SIMILARITY.  
 CC MOD\_RES 382 382 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 CC SEQUENCE 498 AA; 56513 MW; BE49D7B079FDD577 CRC64;  
 SO  
 Query Match 33.7%; Score 97; DB 1; Length 498;  
 Best Local Similarity 41.5%; Pred. No. 0.0013;  
 Matches 22; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87172710; PubMed=3561390;  
 RA Yamashita K., Fukushige S., Senba K., Sukegawa J., Miyajima N.,  
 RA Matubara K.-I., Yamamoto T., Toyoshima K.,  
 RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase  
 RT similar to p56lck".  
 RL Mol. Cell. Biol. 7:237-243 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94171041; PubMed=8125304;  
 RA Rider L.G., Raben N., Miller L., Jelsma C.,  
 RT "The cdna encoding two forms of the lyn protein tyrosine kinase are  
 RT expressed in rat mast cells and human myeloid cells".  
 RL Gene 138:219-222 (1994).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: LYN A (SHOWN HERE) AND LYN B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC  
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 CC  
 CC EMBL; M16038; AAA59540.1; -  
 CC EMBL; M79321; AAB50019.1; -  
 CC PIR; A26719; TYHULY.  
 CC HSPD; P06631; LAD5.  
 CC Genew; HGNC:6735; LYN.  
 CC MIM; 165120; -  
 CC InterPro; IPR000719; Euk\_pkinase.  
 CC InterPro; IPR000980; SH2.  
 CC InterPro; IPR01452; SH3.  
 CC InterPro; IPR01245; Tyr\_pkinase.  
 CC Pfam; PF00017; SH2; 1.  
 CC Pfam; PF00018; SH3; 1.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00452; SH3DOMAIN.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Euk\_pkinase; 1.  
 CC ProDom; PD000066; SH3; 1.  
 CC ProDom; PD000093; SH2; 1.  
 CC SMART; SMO0252; SH2; 1.  
 CC SMART; SMO0326; SH3; 1.  
 CC SMART; SMO0219; TYRC; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE; PS50001; SH2; 1.  
 CC PROSITE; PS50002; SH3; 1.  
 CC Tyrosine-protein kinase; Phosphorylation;  
 CC Myristate; SH2 domain; SH3 domain;  
 CC Palmitate; Lipoprotein; Alternative splicing.  
 CC MYRISTATE (BY SIMILARITY).  
 CC LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 CC LIPID 2 2 PALMITATE (BY SIMILARITY).  
 CC DOMAIN 62 122 SH3.  
 CC DOMAIN 128 225 SH2.  
 CC DOMAIN 246 500 PROTEIN KINASE.  
 CC NP\_BIND 252 260 ATP (BY SIMILARITY).  
 CC BINDING 274 274 ATP (BY SIMILARITY).

FT ACT SITE 366 366 BY SIMILARITY.  
 FT MOD\_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).  
 FT VASPLC 22 42 MISSING (IN ISOFORM LYN B).  
 SO SEQUENCE 511 AA; 58442 MW; 8419CD461204E364 CRC64;

Query Match 33.0%; Score 95; DB 1; Length 511;  
 Best Local Similarity 37.7%; Pred. No. 0.0023;  
 Matches 20; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 4 VALGSPAGPAPLRLGEPPLTVSDGWTWTVLSEVSGREYNIPTSVHVA 56  
 Db 68 VALYVDGHPDLSPKGEKVKVLEHGEWMKXSLTKKEGFIPTSNVAKL 120

RESULT 6  
 SRC2\_XENLA STANDARD; PRT; 531 AA.  
 AC P1316;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase SRC-2 (EC 2.7.1.112) (p60-SRC-2).  
 GN SRC-2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xeropodinae; Xenopus.  
 OK NCBI\_TaxID=8335;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89278134; PubMed=2499582;  
 RA Steele R.E., Unger T.F., Mardis M.J., Fero J.B.;  
 RT "The two Xenopus laevis SRC genes are co-expressed and each produces  
 functional p60src".  
 RL J. Biol. Chem. 264:10649-10653(1989).

RN [2]  
 RP SEQUENCE OF 438-491 FROM N.A.  
 RC TISSUE=Erythrocyte;  
 RX MEDLINE=85215578; PubMed=2987836;  
 RA Steele R.E.;  
 RT "Two divergent cellular src genes are expressed in Xenopus laevis";  
 RL Nucleic Acids Res. 13:1747-1761(1985).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC -1- tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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DR EMBL; M23422; AAA49961.1; -;  
 DR EMBL; M30858; AAA51644.1; -;  
 DR EMBL; M30857; AAA51644.1; JOINED.  
 DR PIR; B34104; B34104.  
 DR HSSP; P00523; 2PTK.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PRO0401; SH2DOMAIN.  
 DR PRINTS; PRO0452; SH3DOMAIN.  
 DR PRINTS; PRO0109; TYRKINASE.

DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00329; Tyrc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00002; SH2; 1.  
 DR PROSITE; PS00001; SH3; 1.  
 KW Transferase; ATP-binding; Tyrosine-protein kinase; Phosphorylation;  
 KW Myristate; SH3 domain; SH2 domain.  
 FT INIT MET 0 0 BY SIMILARITY.  
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 FT DOMAIN 79 140 SH3.  
 FT DOMAIN 146 243 SH2.  
 FT DOMAIN 265 518 PROTEIN KINASE.  
 FT NP\_BIND 271 279 ATP (BY SIMILARITY).  
 FT BINDING 293 293 ATP (BY SIMILARITY).  
 FT ACT\_SITE 384 384 BY SIMILARITY.  
 FT MOD\_RES 414 414 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SO SEQUENCE 531 AA; 59605 MW; ED04ACB8E09C51B CRC64;

Query Match 32.1%; Score 92.5; DB 1; Length 531;  
 Best Local Similarity 44.4%; Pred. No. 0.0046;  
 Matches 24; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

Qy 2 TAVAGSPAGPAPLRLGEPPLTVSE-DGDMWTWVLSREYNIPTSVHVA 54  
 Db 83 TPVALVDYBSRTETDLSFRGRLQIVNNTSGDWMLRLSLSSGQGYIPTSNVA 136

RESULT 7  
 STK\_HYDAT STANDARD; PRT; 509 AA.  
 AC P17713;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase STK (EC 2.7.1.112) (p57-STK).  
 GN STK.  
 OS Hydra attenuata (Hydra) (Hydra vulgaris).  
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;  
 OC Hydrozoa; Hydra.  
 OK NCBI\_TaxID=6087;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90066418; PubMed=2479820;  
 RA Borch T.C.O., Unger T.F., Fisher D.A., Steele R.E.;  
 RT "Structure and expression of STK, a src-related gene in the simple  
 RT metazoan Hydra attenuata".  
 RL Mol. Cell. Biol. 9:4141-4151(1989).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC -1- tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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DR EMBL; M25245; AAA29217.1; -;  
 DR PIR; A34094; TVHAST.  
 DR HSSP; P00523; 1SRL.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.

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DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk pkinase; 1.
DR Prodom: PD000066; SH3; 1.
DR Prodom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50002; SH2; 1.
DR PROSITE: PS50003; SH3; 1.
KW Tyrosine-protein kinase, Proto-oncogene; Phosphorylation;
KW Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT DOMAIN 59 120 SH3.
FT DOMAIN 126 218 SH2.
FT DOMAIN 240 495 PROTEIN_KINASE.
FT NP_BIND 246 254 ATP (BY SIMILARITY).
FT BINDING 268 268 ATP (BY SIMILARITY).
FT ACT_SITE 360 360 BY SIMILARITY.
FT MOD_RES 390 390 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 509 AA; 56885 MW; D061812B35F9953 CRC64;

Query Match 31.4%; Score 90.5; DB 1; Length 509;
Best Local Similarity 42.3%; Pred. No. 0.0074;
Matches 22; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

Cy 4 VALGSPAGPAELSLRLGEPPLTVSSEGGMTVTVSEVSGREYINPSVHAKY 54
Db 65 VALDYEAIRHEDLSFKKGRLOITVADSGMWYAKSLTNSGRTIPSTIYA 116

RESULT 8
ID_HCK_RAT STANDARD; PRT; 503 AA.
AC P50545; Q64647;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
DE kinase).
GN HCK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92109719; PubMed=1764064;
RX Okano Y., Sugimoto Y., Fukuoaka M., Matsui A., Nagata K.I., Nozawa Y.;
RA "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
RT characterization of its gene product.";
RT megakaryocytes";
RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Spleen;
RC Vajaya Gauri B.S., Renna V., Kamathar S., Swarup G.;
RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
RT characterization of its gene product.";
RL J. Biol. 19:117-129(1994).
CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
CC DEGRANULATION PROCESS OF NEUTROPHILS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

```

```

CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTRAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTRAINS 1 SH3 DOMAIN.
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CC -----
CC EMBL: S74141; AA820754.1; -
CC EMBL: M83666; AAA41312.1; -
CC EMBL: X62345; CAA44218.1; -
CC HSSP: P08631; 1BU1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR00117; SH2; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 1.
DR Prodom: PD000066; SH3; 1.
DR Prodom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50002; SH2; 1.
DR PROSITE: PS50003; SH3; 1.
KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Myristate; SH2 domain; SH3 domain.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT DOMAIN 55 115 SH3.
FT DOMAIN 121 218 SH2.
FT DOMAIN 239 492 PROTEIN_KINASE.
FT NP_BIND 245 253 ATP (BY SIMILARITY).
FT BINDING 267 267 ATP (BY SIMILARITY).
FT ACT_SITE 358 358 BY SIMILARITY.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT MOD_RES 388 388 F -> V (IN REF. 2).
FT CONFLICT 51 51 K -> R (IN REF. 2).
FT CONFLICT 205 205 I -> T (IN REF. 2).
FT CONFLICT 306 306 I -> T (IN REF. 2).
SQ SEQUENCE 503 AA; 57016 MW; A1FC1F3F0B82FF73 CRC64;

Query Match 31.2%; Score 90; DB 1; Length 503;
Best Local Similarity 35.8%; Pred. No. 0.0084;
Matches 19; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Cy 4 VALGSPAGPAELSLRLGEPPLTVSSEGGMTVTVSEVSGREYINPSVHAKY 56
Db 61 VALDYEAIRHEDLSFKKGRLOITVADSGMWYAKSLTNSGRTIPSTIYA 113

RESULT 9
ID_HCK_MACFA STANDARD; PRT; 504 AA.
AC Q95M30;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
DE kinase).

```

GN HCK.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_Taxid=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Picard C.;  
RL Thesis (2001), University of Marseille, France.  
CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC  
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO  
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE  
CC DEGRANULATION PROCESS OF NEUTROPHILS (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate  
CC -1- SUBCELLULAR LOCATION: Membrane-associated (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
CC SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -----  
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CC -----  
CC EMBL: AJ320181; CAC44031.1;  
CC Interpro: IPR000719; Euk\_Pkinase.  
CC Interpro: IPR000980; SH2.  
CC Interpro: IPR001452; SH3.  
CC Interpro: IPR001245; Tyr\_Pkinase.  
CC Pfam: PF00017; SH2; 1.  
CC Pfam: PF00018; SH3; 1.  
CC Pfam: PF00069; Pkinase; 1.  
CC Prodom: PD000001; Euk\_Pkinase; 1.  
CC Prodom: PD000066; SH3; 1.  
CC Prodom: PD000093; SH2; 1.  
CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
CC PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
CC PROSITE: PS50001; SH2; 1.  
CC PROSITE: PS50002; SH3; 1.  
CC Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;  
KM Myristate; SH2 domain; SH3 domain.  
FT DOMAIN 56 116  
FT DOMAIN 122 219  
FT DOMAIN 240 493  
FT NP\_BIND 246 254  
FT BINDING 268 268  
FT ACT\_SITE 359 359  
FT LIGAND 2 2  
FT MOD\_RES 389 389  
FT SEQUENCE 504 AA: 57096 MW: 535293222023433 CRC64;  
Query Match 31.2%; Score 90; DB 1; Length 504;  
Best Local Similarity 35.8%; Pred. No. 0.0084;  
Matches 19; Conservative 12; Mismatches 22; Indels 0; Gaps 0;  
OY 4 VALGSPAGPAELSLRLGEPLTVSDQMTVSEVSGEVIPTSVAVAKV 56  
DB 62 VALYDEAIHHEDLSFKQGDQMVVLESGEWMKASLATREKGIISNVAVAV 114  
RESULT 10  
HCK\_HUMAN STANDARD; PRT; 526 AA.  
AC P08631; Q96C00; Q9H5Y5; Q9NUA4; Q9UMJ5;  
AC 01-AUG-1988 (Rel. 08, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (p59-HCK and p60-HCK)  
DE (hemopoietic cell kinase).  
GN HCK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE OF 22-526 FROM N.A.  
RX MEDLINE=87257942; PubMed=3496523;  
RA Quintrell N., Lebo R., Varmus H., Bishop J.M., Pettenati M.J.,  
RA Le Beau M.M., Diaz M.O., Rowley J.D.;  
RT "Identification of a human gene (HCK) that encodes a protein-tyrosine  
RT kinase and is expressed in hemopoietic cells.";  
RL Mol. Cell. Biol. 7:2267-2275 (1987).  
RN [2]  
RP SEQUENCE OF 22-526 FROM N.A.  
RX MEDLINE=87257943; PubMed=3453117;  
RA Ziegler S.F., Marth J.D., Lewis D.B., Perlmutter R.M.;  
RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in  
RT cells of hematopoietic origin.";  
RL Mol. Cell. Biol. 7:2276-2285 (1987).  
RN [3]  
RP SEQUENCE OF 22-526 FROM N.A.  
RC TISSUE-B-cell;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 22-526 FROM N.A.  
RC TISSUE=ileal mucosa;  
RA Kakakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ota T.,  
RA Yamada K., Fujii Y., Ozaki K., Harao M., Omori Y., Ota T., Suzuki Y.,  
RA Ogasawara M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
RA Isogai T., Sugano S.;  
RT "MDO human cDNA sequencing project.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21638749; PubMed=11780052;  
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cobby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,  
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond D.V., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Levasailho M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McComachie L.J., McLeay K., McMurtry A.A.,  
RA Maine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prichallingam S.R., Plumb R.W., Ramay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Seitz H.K., Showkseen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston R.J.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Williams J.M., Thorpe A.,  
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871 (2001).  
RN [6]  
RP SEQUENCE OF 179-526 FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=92241680; PubMed=1572549;  
RA Hradetzky D., Streibhardt K., Ruebsamen-Waigmann H.;



RT "The genomic locus of the human hemopoietic-specific cell protein  
RT tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of  
RT exon-intron structure among human PTKs of the src family.";  
RL Gene 113:275-280(1992).  
RN [7]  
RP SEQUENCE OF 1-22 FROM N.A. AND ALTERNATIVE INITIATION.  
RX MEDLINE=91342636; PubMed=1875927;  
RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;  
RT "Two isoforms of murine hck, generated by utilization of alternative  
RT translational initiation codons, exhibit different patterns of  
RT subcellular localization.";  
RL Mol. Cell. Biol. 11:4363-4370(1991).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.  
RX MEDLINE=97177106; PubMed=9024658;  
RA Sieher F., Moarefi I., Kuriyan J.;  
RT "Crystal structure of the Src family tyrosine kinase Hck.";  
RL Nature 385:602-609(1997).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.  
RX MEDLINE=98453315; PubMed=9778343;  
RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,  
RL Ladbury J.E.;  
RT "RT loop flexibility enhances the specificity of Src family SH3  
RT domains for HIV-1 Nef.";  
RL Biochemistry 37:14683-14691(1998).  
RN [10]  
RP STRUCTURE BY NMR OF 78-138.  
RX MEDLINE=98239731; PubMed=9571048;  
RA Horita D.A., Baldissari D.M., Zhang W., Altieri A.S., Smithgall T.E.,  
RL Gmeiner W.H., Byrd R.A.;  
RT "Solution structure of the human Hck SH3 domain and identification of  
RT its ligand binding site.";  
RL J. Mol. Biol. 278:253-265(1998).  
RN [11]  
RP STRUCTURE BY NMR OF 139-245.  
RX MEDLINE=97263487; PubMed=9109402;  
RA Zhang W., Smithgall T.E., Gmeiner W.H.;  
RT "Sequential assignment and secondary structure determination for the  
RT Src homology 2 domain of hematopoietic cellular kinase.";  
RL FEBS Lett. 406:131-135(1997).  
RN [12]  
RP FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC  
RP RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO  
RP CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE  
RP DEGRANULATION PROCESS OF NEUTROPHILS.  
CC CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH  
CC MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).  
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, P60-HCK (shown here) and P59-  
CC HCK, are produced by alternative initiation.  
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE  
CC MYELOID AND B-LYMPHOID LINEAGES.  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
CC SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL: M16591; AAAS2643.1; -  
DR EMBL: M16592; AAAS2644.1; -  
DR EMBL: BC014435; AAH14435.1; -  
DR EMBL: AK026432; BAB15482.1; -  
DR EMBL: AL049539; CAB75606.1; -  
DR EMBL: X58741; CAA41565.2; -  
DR EMBL: X58742; CAA41565.2; JOINED.

DR EMBL: X58743; CAA41565.2; JOINED.  
DR PIR: A27812; TVHDC.  
DR PDB: 2HCK; 20-AUG-97.  
DR PDB: 3HCK; 15-OCT-97.  
DR PDB: 4HCK; 17-JUN-98.  
DR PDB: 5HCK; 17-JUN-98.  
DR PDB: 1AD5; 15-MAY-97.  
DR PDB: 1BU1; 11-NOV-98.  
DR Gene; HGNC:4840; HCK.  
DR MIM; 142370; -  
DR InterPro: IPR000719; Euk.pkinase.  
DR InterPro: IPR000980; SH2.  
DR InterPro: IPR001452; SH3.  
DR InterPro: IPR002290; Ser.thr.pkinase.  
DR InterPro: IPR001245; Tyr.pkinase.  
DR Pfam; PR00017; SH2; 1.  
DR Pfam; PR00018; SH3; 2.  
DR Pfam; PR00069; pkinase; 4.  
DR ProDom; PD000066; SH3; 1.  
DR ProDom; PD000093; SH2; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 1.  
DR SMART; SM00220; S.TKC; 1.  
DR SMART; SM00219; TYRC; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS50001; SH2; 1.  
DR PROSITE; PS50002; SH3; 1.  
DR Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;  
KW Myristate; SH2 domain; SH3 domain; Alternative initiation;  
KW 3d-structure.  
FT CHAIN 1 526 TYROSINE-PROTEIN KINASE P60-HCK.  
FT INIT MET 22 526 TYROSINE-PROTEIN KINASE P59-HCK.  
FT INIT MET 22 526 FOR ISOFORM P59-HCK.  
FT DOMAIN 78 138 SH3.  
FT DOMAIN 144 241 SH2.  
FT DOMAIN 262 515 PROTEIN KINASE.  
FT NP BIND 268 276 ATP.  
FT BINDING 290 290 ATP.  
FT ACT SITE 381 381 ATP.  
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).  
FT LIPID 23 23 WRISTATE (BY SIMILARITY).  
FT MOD RES 411 411 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CONFLICT 24 24 C -> S (IN REF. 1).  
FT CONFLICT 144 144 W -> R (IN REF. 4).  
SQ SEQUENCE 526 AA; 59599 MW; 847E877A0A641725 CRC64;  
Query Match 31.2%; Score 90; DB 1; Length 526;  
Best Local Similarity 35.8%; Pred. No. 0.0088;  
Matches 19; Conservative 12; Mismatches 22; Indels 0; Gaps 0;  
QY 4 VALGSPAGGPARLSRLRGEPITVSGDGMWTVLSEVSGREYNIPGVAVY 56  
Db 84 VALDYEAHINHDLSFGKQDMVVLSESGEWMKARSLATRGYIPSNVAVY 136  
RESULT 11  
SRC1\_XENLA STANDARD; PRT; 531 AA.  
ID SRC1\_XENLA  
AC P13115;  
DT 01-JAN-1990 (Rel. 13; Created)  
DT 15-JUN-2002 (Rel. 41; Last sequence update)  
DT 15-JUN-2002 (Rel. 41; Last annotation update)  
DE Tyrosine-protein kinase SRC-1 (BC 2.7.1.112) (p60-SRC-1).  
GN SRC-1.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae.  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.



RX MEDLINE=89278134; PubMed=2499582;  
 RA Steele R.E., Unger T.F., Maris M.J., Fero J.B.;  
 RT "The two Xenopus laevis SRC genes are co-expressed and each produces  
 RL J. Biol. Chem. 264:10649-10653(1989).  
 RN [2]  
 RP REVISIONS TO 219; 241 AND 339.  
 RA Steele R.E.;  
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M24704; AAA49962.2; -  
 DR PIR: A34104; A34104.  
 DR HSSP: P00523; 2PTK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0401; SH2DOMAIN.  
 DR PRINTS: PRO0452; SH3DOMAIN.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000066; SH3; 1.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00219; TykK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50011; SH2; 1.  
 DR ProSite: PS50002; SH3; 1.  
 KW Transferase; ATP-binding; Tyrosine-protein kinase; Phosphorylation;  
 KW Myristate; SH3 domain; SH2 domain  
 KW INIT\_MET 0 BY SIMILARITY.  
 FT INIT\_MET 0  
 FT LITID 1  
 FT DOMAIN 79 140  
 FT DOMAIN 146 243  
 FT DOMAIN 265 518  
 FT NP\_BIND 271 279  
 FT BINDING 293 293  
 FT ACT\_SITE 384 384  
 FT MOD\_RES 414 414  
 SQ SEQUENCE 531 AA; 59763 MW; 8397790D6462671 CRC64;  
 Query Match 31.1%; Score 89.5; DB 1; Length 531;  
 Best Local Similarity 42.6%; Pred. No. 0.01;  
 Matches 23; Conservative 8; Mismatches 22; Indels 1; Gaps 1;  
 QY 2 TAVAGSFPAGPAELSLRLGEPITVSE-DGDMWTVSEVSGENIVSSVVA 54  
 DB 83 TFVALDYESTRTDLSEKGERLQIVNTEGDMILARSLSSGGTGITISNYVA 136  
 RESULT 12  
 SPCA\_DROME STANDARD; PRT; 2415 AA.  
 ID SPCA\_DROME PRT; 2415 AA.  
 RT

AC P13395; Q9W085; Q26340;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Spectrin alpha chain.  
 GN ALPHA-SPEC OR SPEC-A OR CG1977.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Insecta; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Muscophora; Ephydroidea; Drosophilidae; Drosophila.  
 OK NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90037215; PubMed=2808524;  
 RA Dubreuil R.R., Byers T.J., Sillman A.L., Bar-Zvi D.,  
 RA Goldstein L.S.B., Branton D.;  
 RT "The complete sequence of Drosophila alpha-spectrin: conservation of  
 RL structural domains between alpha-spectrins and alpha-actinin.";  
 RN J. Cell Biol. 109:2197-2205(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutcliffe G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brannon R.C., Rogers Y.-H.C., Blake J.R., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,  
 RA Borkov D., Borchen M.R., Bouck P., Brockstein P., Brotter P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honick J.,  
 RA Hostin D., Houston K.A., Howland T.O., Wei M.-H., Ibegwan C.,  
 RA Jatalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Maltsev B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tecor C., Turner C., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodedge T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu G., Zhu H.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP SEQUENCE OF 1-150 AND 2192-2415 FROM N.A., AND CHARACTERIZATION.  
 RN MEDLINE=9410334; PubMed=8276898;  
 RX Lee J.K., Coyne R.S., Dubreuil R.R., Goldstein L.S.B., Branton D.,  
 RT "Cell shape and interaction defects in alpha-spectrin mutants of  
 RL Drosophila melanogaster.";  
 RN J. Cell Biol. 123:1797-1809(1993).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=88059242; PubMed=3680372;  
 RA Dubreuil R., Byers T.J., Branton D., Goldstein L.S.B., Kiehart D.P.,  
 RT "Drosophila spectrin. I. Characterization of the purified protein.";  
 RN

FT	REPEAT	441	546	SPECTRIN 5.
FT <th>REPEAT</th> <td>547</td> <td>651</td> <th>SPECTRIN 6.</th>	REPEAT	547	651	SPECTRIN 6.
FT <th>REPEAT</th> <td>652</td> <td>757</td> <th>SPECTRIN 7.</th>	REPEAT	652	757	SPECTRIN 7.
FT <th>REPEAT</th> <td>758</td> <td>863</td> <th>SPECTRIN 8.</th>	REPEAT	758	863	SPECTRIN 8.
FT <th>REPEAT</th> <td>864</td> <td>969</td> <th>SPECTRIN 9.</th>	REPEAT	864	969	SPECTRIN 9.
FT <th>REPEAT</th> <td>970</td> <td>1043</td> <th>SPECTRIN 10.</th>	REPEAT	970	1043	SPECTRIN 10.
FT <th>REPEAT</th> <td>1044</td> <td>1151</td> <th>SPECTRIN 11.</th>	REPEAT	1044	1151	SPECTRIN 11.
FT <th>REPEAT</th> <td>1152</td> <td>1257</td> <th>SPECTRIN 12.</th>	REPEAT	1152	1257	SPECTRIN 12.
FT <th>REPEAT</th> <td>1258</td> <td>1363</td> <th>SPECTRIN 13.</th>	REPEAT	1258	1363	SPECTRIN 13.
FT <th>REPEAT</th> <td>1364</td> <td>1469</td> <th>SPECTRIN 14.</th>	REPEAT	1364	1469	SPECTRIN 14.
FT <th>REPEAT</th> <td>1470</td> <td>1576</td> <th>SPECTRIN 15.</th>	REPEAT	1470	1576	SPECTRIN 15.
FT <th>REPEAT</th> <td>1577</td> <td>1682</td> <th>SPECTRIN 16.</th>	REPEAT	1577	1682	SPECTRIN 16.
FT <th>REPEAT</th> <td>1683</td> <td>1788</td> <th>SPECTRIN 17.</th>	REPEAT	1683	1788	SPECTRIN 17.
FT <th>REPEAT</th> <td>1789</td> <td>1894</td> <th>SPECTRIN 18.</th>	REPEAT	1789	1894	SPECTRIN 18.
FT <th>REPEAT</th> <td>1895</td> <td>2001</td> <th>SPECTRIN 19.</th>	REPEAT	1895	2001	SPECTRIN 19.
FT <th>REPEAT</th> <td>2002</td> <td>2115</td> <th>SPECTRIN 20.</th>	REPEAT	2002	2115	SPECTRIN 20.
FT <th>REPEAT</th> <td>2116</td> <td>2229</td> <th>SPECTRIN 21.</th>	REPEAT	2116	2229	SPECTRIN 21.
FT <th>REPEAT</th> <td>2230</td> <td>2335</td> <th>SPECTRIN 22.</th>	REPEAT	2230	2335	SPECTRIN 22.
FT <th>CA BIND</th> <td>2278</td> <td>2289</td> <th>EF-HAND 1 (POTENTIAL).</th>	CA BIND	2278	2289	EF-HAND 1 (POTENTIAL).
FT <th>CA BIND</th> <td>2321</td> <td>2332</td> <th>EF-HAND 2 (POTENTIAL).</th>	CA BIND	2321	2332	EF-HAND 2 (POTENTIAL).
FT <th>DOMAIN</th> <td>970</td> <td>1029</td> <th>SH3.</th>	DOMAIN	970	1029	SH3.
FT <th>CONFLICT</th> <td>110</td> <td>110</td> <td>Q -&gt; D (IN REF. 3).</td>	CONFLICT	110	110	Q -> D (IN REF. 3).
FT <th>CONFLICT</th> <td>168</td> <td>168</td> <td>Q -&gt; R (IN REF. 1).</td>	CONFLICT	168	168	Q -> R (IN REF. 1).
SEQ <th>SEQUENCE</th> <td>2415 AA;</td> <td>278301 MM;</td> <td>F1172FB90EB0A37 CRC64;</td>	SEQUENCE	2415 AA;	278301 MM;	F1172FB90EB0A37 CRC64;
Query Match		31.1%;	Score 89.5;	DB 1; Length 2415;
Best Local Similarity		35.2%;	Pred. No. 0.05;	
Matches 19;	Conservative 15;	Mismatches 17;	Indels 3;	Gaps 2
DB	976 VALSPAGCPALSLRIGRELTVLSDGGMWTVLSEVSGRENNISGVAVK 56			
	4 VALSPAGCPALSLRIGRELTVLSDGGMWTVLSEVSGRENNISGVAVK 56			
	976 VALDYTKSPREVSWKGGVLTLLSNKKMKMRV-EVNDKRGVPMAYIKKI 1027			
RESULT 13				
LCK_CHICK				
ID_LCK_CHICK	STANDARD;	PRT;	507 AA.	
P42683;				
DT 01-NOV-1995 (Rel. 32, Created)				
DT 01-NOV-1995 (Rel. 32, Last sequence update)				
DT 15-VUN-2002 (Rel. 41, Last annotation update)				
DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TXL).				
DE LCK.				
GN Gallus gallus (Chicken).				
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
NCBI_TaxID=9031;				
ON (1)				
SEQUENCE OF 1-88 FROM N.A.				
RX MEDLINE=8097370; PubMed=1545804;				
RX MEDLINE=9216854; PubMed=1545804;				
RA Chow L., Ratcliffe M., Veillette A., "tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene."				
RT Mol. Cell. Biol. 12:1226-1233 (1992).				
RL (2)				
SEQUENCE OF 46-507 FROM N.A.				
RX MEDLINE=88097370; PubMed=3321053;				
RA Streibhardt K., Mullins J.I., Bruck C., Ruebsaen-Wajsmann H., "Additional member of the protein-tyrosine kinase family: the src-RT and lck-related protooncogene c-tyl."				
RT Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782 (1987).				
CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.				
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.				
CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CD4 OR CD8.				
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.				
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.				
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.				

Q	SEQUENCE	507 AA; 58008 MW; EC3JCAF69J1B6170 CRC64;
DR	EMBL; M85043; AAA49003.1; "	
DR	EMBL; J03579; AAA49081.1; ALT_INIT.	
DR	HSSP; P06239; 3ICK.	
DR	InterPro; IPR000719; Euk_Pkinase.	
DR	InterPro; IPR000980; SH2.	
DR	InterPro; IPR001452; SH3.	
DR	InterPro; IPR001245; Tyr_pkinase.	
DR	Pfam; PF00017; SH2; 1.	
DR	Pfam; PF00018; SH3; 1.	
DR	Pfam; PF00069; pkinase; 1.	
DR	PRINTS; PR00401; SH2DOMAIN.	
DR	PRINTS; PR00452; SH3DOMAIN.	
DR	PRINTS; PR00109; TYRKINASE.	
DR	ErdDom; PD000001; Euk_Pkinase; 1.	
DR	ErdDom; PD000066; SH3; 1.	
DR	ErdDom; PD000093; SH2; 1.	
DR	SMART; SMO0252; SH2; 1.	
DR	SMART; SMO0326; SH3; 1.	
DR	SMART; SMO0219; TyKc; 1.	
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.	
DR	PROSITE; PS00109; PROTEIN KINASE TYR; 1.	
DR	PROSITE; PSS0011; PROTEIN KINASE_DOM; 1.	
DR	PROSITE; PSS0001; SH2; 1.	
DR	PROSITE; PSS0002; SH3; 1.	
KW	Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;	
KW	ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;	
KM	LiPpocketing.	
FT	INIT MET	0 0
FT	LIPID	1 1
FT	LIPID	2 2
FT	LIPID	4 4
FT	LIPID	59 119
FT	DOMAIN	125 222
FT	DOMAIN	243 496
FT	NP_BIND	249 257
FT	ACT BINDING	271 271
FT	ACT SITE	362 362
FT	MOD_RES	392 392
FT	MOD_RES	503 503
Q	SEQUENCE	507 AA; 58008 MW; EC3JCAF69J1B6170 CRC64;

RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE=89123626; PubMed=3365417;  
 RX Perlmuter R.M., March J.D., Lewis D.B., Peet R., Ziegler S.F.,  
 RA Wilson C.B.;  
 RT "structure and expression of lck transcripts in human lymphoid  
 RL cells.";  
 RN J. Cell. Biochem. 38:117-126(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87133831; PubMed=3493153;  
 RA Koga Y., Caccia N., Toyonaga B., Spolaki R., Yanagi Y., Yoshikai Y.,  
 RA Mck T.W.;  
 RT "A human T cell-specific cDNA clone (YT1c) encodes a protein with  
 RL extensive homology to a family of protein-tyrosine kinases.";  
 RN Eur. J. Immunol. 16:1643-1646(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90108697; PubMed=2558056;  
 RA Rouet E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,  
 RA Benarous R.;  
 RT "Structure of the human lck gene: differences in genomic organisation  
 RL within src-related genes affect only N-terminal exons.";  
 RN Gene 84:105-113(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A. VARIANTS L-27; POKP-231 INS, V-352, L-446, AND  
 RX PHOSPHORYLATION OF TYR-393 AND TYR-504.  
 RN TISSUE=leukemia;  
 RX MEDLINE=94187714; PubMed=8139546;  
 RA Wright D.D., Setton B.M., Kampes M.P.;  
 RT "Oncogenic activation of the lck protein accompanies translocation o  
 RL the LCK gene in the human HS27 T-cell leukemia.";  
 RN Mol. Cell. Biol. 14:2429-2437(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RX TISSUE=leukemic T-cell;  
 RX MEDLINE=96085119; PubMed=7495859;  
 RA Vogel L.B., Arthur R., Fujita D.O.;  
 RT "An aberrant lck mRNA in two human T-cell lines.";  
 RL Biochim. Biophys. Acta 1264:168-172(1995).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Lymph;  
 RA Straussberg R.;  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 13-508 FROM N.A.  
 RX TISSUE=Peritoneal blood lymphocytes;  
 RA MEDLINE=20462621; PubMed=11009097;  
 RA Boncristiano M.B., Mojilini M.B., D'Elia M.M., Pacini S., Valensin S.,  
 RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,  
 RA Baldari C.T.;  
 RT "Defective recruitment and activation of ZAP-70 in common variable  
 RL immunodeficiency patients with T cell defects.";  
 RN Eur. J. Immunol. 30:2632-2638(2000).  
 RN [8]  
 RP SEQUENCE OF 367-508 FROM N.A.  
 RX MEDLINE=88217332; PubMed=2835736;  
 RA Veillette A., Foss F.M., Sauvaille E.A., Bolen J.B., Rosen N.;  
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma  
 RL and other non-lymphoid human tumor cell lines.";  
 RN Oncogene Res. 1:357-374(1987).  
 RN [9]  
 RP SEQUENCE OF 374-508 FROM N.A.  
 RX MEDLINE=87000726; PubMed=389486;  
 RA Trevillian J.M., Lin Y., Chen S.J., Philippe C.A., Canna C.,  
 RA Lima T.J.;  
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to  
 RL p56LCK.";  
 RN Biochim. Biophys. Acta 888:286-295(1986).  
 RN [10]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE=89096891; PubMed=2850479;

RA Garvin A.M., Pawar S., March J.D., Perlmuter R.M.;  
 RT "Structure of the murine lck gene and its rearrangement in a murine  
 RT lymphoma cell line.";  
 RL Mol. Cell. Biol. 8:3058-3064(1988).  
 RN [11]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RA MEDLINE=89313764; PubMed=2787474;  
 RA Takadera T., Leung S., Geronzi A., Koga Y., Takihara Y.,  
 RA Miyamoto N.G., Mak T.W.;  
 RT "Structure of the two promoters of the human lck gene: differential  
 RT accumulation of two classes of lck transcripts in T cells.";  
 RL Mol. Cell. Biol. 9:2173-2180(1989).  
 RN [12]  
 RP MASS SPECTROMETRY.  
 RC TISSUE=breast cancer;  
 RX MEDLINE=21829512; PubMed=11840567;  
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,  
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,  
 RA Zvelebil M.J.;  
 RT "Cluster analysis of an extensive human breast cancer cell line  
 RT protein expression map database.";  
 RL Proteomics 2:212-223(2002).  
 RN [13]  
 RP INTERACTION WITH PI3K.  
 RX MEDLINE=94067101; PubMed=7504174;  
 RA Vogel L.B., Fujita D.J.;  
 RT "The SH3 domain of p56lck is involved in binding to  
 RT phosphatidylinositol 3'-kinase from T lymphocytes.";  
 RL Mol. Cell. Biol. 13:7408-7417(1993).  
 RN [14]  
 RP INTERACTION WITH KDRBS1.  
 RX MEDLINE=9515308; PubMed=7852312;  
 RA Vogel L.B., Fujita D.J.;  
 RT "p70 phosphorylation and binding to p56lck is an early event in  
 RT interleukin-2-induced onset of cell cycle progression in  
 RT T-lymphocytes.";  
 RL J. Biol. Chem. 270:2506-2511(1995).  
 RN [15]  
 RP PHOSPHORYLATION OF TYR-504.  
 RX MEDLINE=92347326; PubMed=1639064;  
 RA Bergman K.E., Muscetto T., Oetken C., Partanen J., Flint N.A.,  
 RA Amrein K.E., Autero M., Burn P., Alitalo K.;  
 RT "The human p50cck tyrosine kinase phosphorylates p56lck at Tyr-505 and  
 RT down regulates its catalytic activity.";  
 RL EMBO J. 11:2919-2924(1992).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.  
 RX MEDLINE=94203291; PubMed=7512222;  
 RA Beck M.J., Atweil S.K., Shoelson S.E., Harrison S.C.;  
 RT "Structure of the regulatory domains of the Src-family tyrosine  
 RT kinase Lck.";  
 RL Nature 368:764-769(1994).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.  
 RX MEDLINE=95173978; PubMed=7532720;  
 RA Mkol V., Baumann G., Keller T.H., Manning U.M., Zurini M.G.M.;  
 RT "The crystal structures of the SH2 domain of p56lck complexed with  
 RT two phosphopeptides suggest a gated peptide binding site.";  
 RL J. Mol. Biol. 246:344-355(1995).  
 RN [18]  
 RP X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 121-225.  
 RX MEDLINE=96177765; PubMed=8604142;  
 RA Tong L., Warren T.C., King U., Betageri R., Rose J., Jakes S.;  
 RT "Crystal structures of the human p56lck SH2 domain in complex with  
 RT two short phosphotyrosyl peptides at 1.0-A and 1.8-A resolution.";  
 RL J. Mol. Biol. 256:601-610(1996).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 118-225.  
 RX MEDLINE=98352059; PubMed=9665372;  
 RA Tong L., Warren T.C., Lukas S., Schambri-King U., Betageri R.,  
 RA Proudfoot J.R., Jakes S.;  
 RT "Carboxymethyl-phenylalanine as a replacement for phosphotyrosine in  
 RT SH2 domain binding.";

RL J. Biol. Chem. 273:20238-20242(1998).  
 RN [20]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500.  
 RX MEDLINE=97100952; PubMed=8945479;  
 RA Yamaguchi H., Hendrickson W.A.;  
 RT "Structural basis for activation of human lymphocyte kinase Lck upon  
 RT tyrosine phosphorylation.";  
 RL Nature 384:484-489(1996).  
 RN [21]  
 RP FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: Binds to phosphatidylinositol 3'-kinase (PI3K) from T  
 CC lymphocytes through its SH3 domain and to the tyrosine  
 CC phosphorylated form of KDRBS1/p70 through its SH2 domain.  
 CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOSOL/MEMBRANE DOMAIN OF EITHER  
 CC CD4 OR CD8.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a  
 CC short form; may be produced by alternative splicing.  
 CC -1- MASS SPECTROMETRY: Mw=57869.42; METHOD=MALDI.  
 CC -1- DISEASE: Involved in leukemias by a chromosomal translocation  
 CC t(1;7)(p34;q34) which involves Lck and T-cell receptor beta chain  
 CC (TCRB) genes.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC or send an email to [license@isb-stb.ch](mailto:license@isb-stb.ch)).  
 DR EMBL: X13529; CAA31884.1; -;  
 DR EMBL: M36881; AAA59502.1; -;  
 DR EMBL: X04476; CAA28165.1; -;  
 DR EMBL: X14053; CAA32211.1; -;  
 DR EMBL: X14053; CAA32211.1; JOINED.  
 DR EMBL: X14054; CAA32211.1; JOINED.  
 DR EMBL: U07236; AAA18225.1; -;  
 Query Match 30.6%; Score 88; DB 1; Length 508;  
 Best Local Similarity 36.5%; Pred. No. 0.014;  
 Matches 19; Conservative 8; Mismatches 25; Indels 0; Gaps 0;  
 QY 4 VALGSPAGPAELSLRGEPLTVSDDGMWTVLSEVSGREINIPSHVAK 55  
 ID LCK\_MOUSE STANDARD; PRT; 508 AA.  
 AC P06240; G61794; G61795; G62320;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (P56-LCK)  
 DE (LCK)  
 GN LCK OR LSK-T.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86079521; PubMed=2416464;  
 RA March J.D., Peet R., Krebs E.G., Perlmuter R.M.;  
 RT "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and  
 RT overexpressed in the murine T cell lymphoma LSTRA.";  
 RL Cell 43:393-404(1985).

RN [2] SEQUENCE FROM N.A.  
 RP MEDLINE=86146842; PubMed=3081813;  
 RA Voronova A.F., Sefton B.M.;  
 RT "Expression of a new tyrosine protein kinase is stimulated by  
 RT retrovirus promoter insertion."  
 RL Nature 319:682-685(1986).  
 RN [3]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RP MEDLINE=89096891; PubMed=2850479;  
 RA Garvin A.M., Pawar S., March J.D., Perlmuter R.M.;  
 RT "Structure of the murine lck gene and its rearrangement in a murine  
 RT lymphoma cell line."  
 RL Mol. Cell. Biol. 8:3058-3064(1988).  
 RN [4]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RP MEDLINE=88142832; PubMed=3501824;  
 RA Voronova A.F., Adler H.T., Sefton B.M.;  
 RT "Two lck transcripts containing different 5' untranslated regions are  
 RT present in T cells."  
 RL Mol. Cell. Biol. 7:4407-4413(1987).  
 RN [5]  
 RP MUTAGENESIS OF TYR-504.  
 RP MEDLINE=88248001; PubMed=3380790;  
 RA Amrein K.E., Sefton B.M.;  
 RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:  
 RT translational basis for virus host-range restriction."  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).  
 RN [6]  
 RP MUTAGENESIS.  
 RP MEDLINE=93059694; PubMed=1279202;  
 RA Hurley T.R., Amrein K.E., Sefton B.M.;  
 RT "Creation and characterization of temperature-sensitive mutants of  
 RT the lck tyrosine protein kinase."  
 RL J. Virol. 66:7406-7413(1992).  
 RN [7]  
 RP MUTAGENESIS OF LYS-272.  
 RP MEDLINE=91163633; PubMed=1706070;  
 RA Abraham N., Miceli M.C., Parnes J.C., Vellente A.;  
 RT "Enhancement of T-cell responsiveness by the lymphocyte-specific  
 RT tyrosine protein kinase p56lck."  
 RL Nature 350:62-66(1991).  
 RN [8]  
 RP MUTAGENESIS OF TYR-504.  
 RP MEDLINE=91219495; PubMed=1708890;  
 RA Abraham K.M., Levin S.D., March J.D., Forbush K.A., Perlmuter R.M.;  
 RT "Thymic tumorigenesis induced by overexpression of p56lck."  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).  
 RN [9]  
 RP MUTAGENESIS.  
 RP MEDLINE=91339805; PubMed=8421674;  
 RA Carrera A.C., Alexandrov K., Roberts T.M.;  
 RT "The conserved lysine of the catalytic domain of protein kinases is  
 RT actively involved in the phosphotransfer reaction and not required  
 RT for anchoring ATP."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).  
 RN [10]  
 RP PALMITOYLATION.  
 RP MEDLINE=94019312; PubMed=8413237;  
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;  
 RT "Palmitoylation of an amino-terminal cysteine motif of protein  
 RT tyrosine kinases p56lck and p59fyn mediates interaction with  
 RT glycosyl-phosphatidylinositol-anchored proteins."  
 RL Mol. Cell. Biol. 13:6385-6392(1993).  
 RN [11]  
 RP PALMITOYLATION.  
 RP MEDLINE=95071286; PubMed=7980442;  
 RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;  
 RT "Palmitoylation of multiple Src-family kinases at a homologous N-  
 RT terminal motif."  
 RL Biochem. J. 303:749-753(1994).  
 CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.  
 CC ITS EARLY EXPRESSION IS ESSENTIAL FOR EARLY T-LYMPHOCYTE

CC DEVELOPMENT.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER  
 CC CD4 OR CD8.  
 CC -1- TISSUE SPECIFICITY: PRESENT AT A LOW LEVEL IN MOST T CELLS, AND  
 CC AT AN ELEVATED LEVEL IN LSTRA AND THY 19 (T-CELL LYMPHOMA) CELLS.  
 CC -1- DEVELOPMENTAL STAGE: LEVELS REMAIN RELATIVELY CONSTANT THROUGHOUT  
 CC T-CELL ONTOGENY.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC -----  
 CC EMBL: X03533; CAA27234.1; -;  
 CC EMBL: M12056; AAB59674.1; -;  
 CC EMBL: X03533; CAA27235.1; ALT\_SEQ.  
 CC EMBL: X03533; CAA27236.1; ALT\_SEQ.  
 CC EMBL: M21511; AAB39422.1; ALT\_SEQ.  
 CC EMBL: M18098; AAB39421.1; -;  
 CC PIR: A23639; A23639.  
 CC HSSP: P06239; 1LCK.  
 CC MGD: MGI:96756; LCK.  
 CC InterPro: IPR000719; Euk\_pkinase.  
 CC InterPro: IPR000980; SH2.  
 CC InterPro: IPR001452; SH3.  
 CC InterPro: IPR001245; Tyr\_pkinase.  
 CC Pfam: PF00017; SH2; 1.  
 CC Pfam: PF00018; SH3; 1.  
 CC Pfam: PF00069; pkinase; 1.  
 CC PRINTS: PR00401; SH2DOMAIN.  
 CC PRINTS: PR00452; SH3DOMAIN.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC PRODOM: PD000001; Euk\_pkinase; 1.  
 CC PRODOM: PD000066; SH3; 1.  
 CC PRODOM: PD000093; SH2; 1.  
 CC SMART: SM00252; SH2; 1.  
 CC SMART: SM00326; SH3; 1.  
 CC SMART: SM00219; Tyrc; 1.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE: PS50001; SH2; 1.  
 CC PROSITE: PS50002; SH3; 1.  
 CC KX ATp-binding; Tyrosine-protein kinase; Phosphorylation; Transferase;  
 CC KX ATp-binding; Myristate; SH2 domain; SH3 domain; Palmitate;  
 CC Lipoprotein.  
 CC FT INIT MET 0 0 PROBABLE.  
 CC FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 CC FT LIPID 2 2 PALMITATE.  
 CC FT LIPID 4 4 PALMITATE.  
 CC FT DOMAIN 60 120 SH2.  
 CC FT DOMAIN 126 223 SH3.  
 CC FT DOMAIN 244 497 PROTEIN KINASE.  
 CC FT NP BIND 250 258 ATP (BY SIMILARITY).  
 CC FT BINDING 272 272 ATP (BY SIMILARITY).  
 CC FT ACT SITE 363 363 BY SIMILARITY.  
 CC FT MOD\_RES 393 393 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 CC FT MOD\_RES 504 504 PHOSPHORYLATION (NEGATIVE REGULATION) (BY  
 CC SIMILARITY).  
 CC FT MUTAGEN 268 268 K->N: REDUCED ACTIVITY.  
 CC FT MUTAGEN 269 269 V->L: REDUCED ACTIVITY.  
 CC FT MUTAGEN 270 270 A->S: REDUCED ACTIVITY.  
 CC FT MUTAGEN 271 271 V->A: REDUCED ACTIVITY.  
 CC FT MUTAGEN 272 272 K->R: LOSS OF ACTIVITY.

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FT	MUTAGEN	273	273	S->N, REDUCED ACTIVITY.
FT	MUTAGEN	274	274	L->M, REDUCED ACTIVITY.
FT	MUTAGEN	275	275	K->N, REDUCED ACTIVITY.
FT	MUTAGEN	504	504	Y->Z CAUSES THYMIC TUMORS
FT	CONFLICT	282	283	VP -> DA (IN REF. 2).
SQ	SEQUENCE	508 AA;	57821 MW;	B25524298C67678 CRC64;

Query Match	30.6%	Score 88;	DB 1;	Length 508;
Best Local Similarity	36.5%	Pred. No. 0.014;		
Matches 19;	Conservative	8;	Mismatches 25;	Indels 0;
			Gaps	0;

OY    4 VALGSFPAGPAELSLRLGEPLTVSDEGDMWTVLSEVSGREYNIPSVHVAK 55  
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Db   66 IALHSYEPRHGDGLGFEEKGEQLRLLDQSGEWWKAQSLTTGGEGFIPFNFAK 117

Search completed: March 24, 2003, 15:46:10  
Job time : 3.37576 secs